37 (New). The mixture according to claim 35, comprising a mixture of Lys/Leu 12-mer peptide diastereomers.

REMARKS

Claims 1-14, 20, 21, 27-35 and 37 presently appear in this case. All of the claims have been allowed subject to elimination of non-elected subject matter. Prosecution on the merits has been closed in accordance with the practice under *Ex parte Quayle*. Reconsideration and passage to issue are hereby respectfully urged.

The examiner notes that applicants have argued that the directive to cancel claim 19 was in error. However, the examiner states that in order to make the record clear, claim 19 should be deleted and a new claim added that has the same subject matter.

In accordance with the examiner's suggestion, claim 19 has now been deleted in favor of new claim 37, in which the subject matter of claim 19 was repeated.

The examiner states that the elected claims are allowable to the extent that they encompass elected subject matter. The examiner now seeks the elimination of non-elected subject matter, specifically, amending the claims to eliminate any possibility of a peptide (or mixtures of peptides) being encompassed which consist of only L-amino acids. The examiner also requires elimination of genus G2.

The claims have now been amended in order to eliminate the non-elected species. Furthermore, the claims

have been reviewed in order to correct any informalities that have been noted, such as improper Markush groups, redundant language and improper punctuation, in order to place all of the claims into better condition for issue. However, other than eliminating non-elected subject matter, it is not believed that any of the changes to the claims are substantive and, thus, all should be considered and entered at this stage of the prosecution.

The amendment of the claims to eliminate non-elected subject matter and the deletion of non-elected claims are expressly made without prejudice toward the continuation of prosecution thereof in a divisional application.

It is submitted that the present application is now in condition for issuance. Prompt issuance of a Notice of Allowance is, therefore, earnestly solicited.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Respectfully submitted,

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Version with Markings to Show Changes Made

1 (~~Twice~~Thrice-Amended). A non-hemolytic cytolytic peptide having a selective cytolytic activity manifested in that it has a cytolytic activity on pathogenic cells, said pathogenic cells being cells which are non-naturally occurring within the body consisting of microbial pathogenic organisms and malignant cells; and it is non-hemolytic, namely it has no cytolytic effect on red blood cells or has a cytolytic effect on red blood cells at concentrations which are substantially higher than that in which it manifests said cytolytic activity on pathogenic cells, said non-hemolytic cytolytic peptide being selected from the group consisting of:

(A) a cyclic derivative of a peptide having a net positive charge which is greater than +1, and comprising both L-amino acid residues and D-amino acid residues, or comprising ~~one or both of L-amino acid residues and~~ only D-amino acid residues, and comprising an α-helix breaker moiety;

(B) a peptide comprising both L-amino acid residues and D-amino acid residues, having a net positive charge which is greater than +1, and having a sequence of amino acids such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature, and cyclic derivatives thereof; and

~~(C) a complex consisting of a plurality of 2 or more non-hemolytic cytolytic peptides, each peptide having a net positive charge which is greater than +1, and comprising both L-amino acid residues and D-amino acid residues, or comprising one or both of L-amino acid residues and D-amino acid residues and comprising an α-helix breaker moiety, or cyclic derivatives of the foregoing, said peptides being linked together by the use of a linker molecule covalently bound to each of the peptides; and~~

(~~D~~C) a random copolymer consisting of a hydrophobic, a positively charged and a D-amino acid.

2 (Amended). ~~The~~ A cyclic peptide according to claim 1(~~1~~A), ~~comprising both D- and L-amino acid residues having a sequence that a homogeneous open-chain peptide comprising only L- or only D-amino acid residues and having the same amino acid sequence as said peptide, has an α-helix configuration and has a broad spectrum cytolytic activity manifested on a variety of cells~~.

6 (~~Twice~~Thrice-amended). ~~The~~ A cyclic peptide according to claim 1, selected from the group of cyclic pardaxin-derived peptides consisting of the herein designated peptides **86-88** (SEQ ID NOs: 86-88, respectively), of the sequence:

86.) Cyclic K^1[D]P^7 $L^{18}L^{19}$ [1-22]-par of the sequence:

Cys-Lys-Gly-Phe-Phe-Ala-Leu-Ile-**Pro**-Lys-Ile-Ile-Ser-
Ser-Pro-Leu-Phe-Lys-Thr-**Leu-Leu**-Ser-Ala-Val-Cys,

87.) Cyclic K^1 K^2[D]P^7 $L^{18}L^{19}$ [1-22]-par of the sequence:

Cys-Lys-Lys-Gly-Phe-Phe-Ala-Leu-Ile-**Pro**-Lys-Ile-Ile-Ser-
Ser-Pro-Leu-Phe-Lys-Thr-Leu-Leu-Ser-Ala-Val-Cys, and

88.) Cyclic K^1 K^2K^3 [D]P^7 $L^{18}L^{19}$ [1-22]-par of the sequence:

Cys-Lys-Lys-Lys-Gly-Phe-Phe-Ala-Leu-Ile-**Pro**-Lys-Ile-Ile-
Ser-Ser-Pro-Leu-Phe-Lys-Thr-**Leu-Leu**-Ser-Ala-Val-Cys.

7 (Twice-Amended). ~~The~~ A peptide according to claim 1 (B), ~~comprising both L-amino acid residues and D-amino acid residues and having a sequence of amino acids such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature~~.

9 (Amended). The peptide according to claim 8, wherein the positively charged amino acid is selected from the group consisting of lysine, arginine and histidine, and the hydrophobic amino acid is selected from the group consisting of leucine, isoleucine, glycine, alanine, valine, phenylalanine, proline, tyrosine and tryptophan.

11 (Amended). The peptide according to claim 10, having at least 6 amino acid residues, in which the hydrophobic amino acid is leucine, alanine or valine, and the positively charged amino acid is lysine.

12 (Amended). The peptide according to claim 11, being a diastereomer of a 6-mer, 8-mer or 12-mer peptide composed of leucine and lysine, in which at least one third of the sequence is composed of D-amino acids, but excepting the peptide herein designated 23 (SEQ ID NO:23):

23) Lys-Leu-**Leu-Leu**-Lys-Leu-Leu-**Leu**-Lys-**Leu**-Leu-Lys-NH_2.

13 (Amended). A Leu/Lys diastereomer according to claim 12, selected from the group of peptides consisting of those herein designated 24 to 29 (SEQ ID NO:24-29, respectively), of the sequence:

24) Lys-Leu-**Leu-Leu**-Lys-Leu-Lys-**Leu**-Lys-**Leu**-Leu-Lys-NH_2,

25) Lys-Lys-**Leu-Leu**-Lys-Leu-Lys-**Leu**-Lys-**Leu**-Lys-Lys-NH_2,

26) **Lys-Leu**-Leu-Leu-**Lys-Leu-Leu**-Leu-**Lys**-Leu-**Leu-Lys**-NH_2,

27) **Lys-Leu**-Leu-Leu-**Lys-Leu-Lys**-Leu-**Lys**-Leu-**Leu-Lys**-NH_2,

28) Lys-**Leu**-Leu-**Leu**-Leu-Lys, and

29) Lys-**Leu**-Leu-**Leu**-Lys-**Leu**-Leu-Lys.

14 (~~Thrice~~Four Times-Amended). ~~The~~ A cyclic derivative of a non-natural synthetic peptide according to claim 7, selected from the group of peptides consisting of

those herein designated 92-95 (SEQ ID NOS:92-95, respectively), of the sequence:

92. Cyclic Cys Lys Leu **Leu** **Leu** Lys Leu Leu **Leu** Lys Leu Leu Lys Cys,

93. Cyclic Cys Lys Leu **Leu** **Leu** Lys Leu Lys **Leu** Lys **Leu** Lys Cys,

94. HN - Lys Leu **Leu** **Leu** Lys Leu Leu **Leu** Lys **Leu** Leu Lys - CO, and

95. HN - Lys Leu Leu Leu Lys Leu Lys Leu Lys Leu Leu Lys - CO.

20 (~~Twice~~Thrice-Amended). ~~The~~ A non-hemolytic cytolytic random copolymer according to claim 1 (~~D~~C), ~~consisting of different ratios of a hydrophobic, a positively charged and a D-amino acid~~.

21 (Amended). The non-hemolytic cytolytic random copolymer according to claim 20, ~~composed~~ consisting of lysine, leucine and D-leucine in the ratio 1:1:1, 2:1:1 or 3:1:1 (Mol).

34 (~~Once~~Twice-Amended). A mixture consisting of two or more non-hemolytic cytolytic peptides or cyclic derivatives thereof, each peptide or derivative having a net positive charge which is greater than +1 and comprising both L-amino acid residues, and D-amino acid residues, or ~~each peptide~~

comprising ~~one or both of L-amino acid residues and~~ only D-amino acid residues and comprising an α-helix breaker moiety.

35 (~~New~~Amended). The mixture of claim 34, wherein each peptide or derivative present in the mixture consists of 12 amino acids, each of which is selected from the group consisting of L-Leu, D-Leu, L-Lys, and D-Lys.

Claims 15-17, 19 and 36 have been deleted.

New claim 37 has been added.